

# Seq ID NO:2 against mouse Doc4

## RESULT 1

T14271

Doc4 protein, stress-induced - mouse

N;Alternate names: odz protein homolog

C;Species: Mus musculus (house mouse)

C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999

C;Accession: T14271

R;Wang, X.Z.; Kuroda, M.; Sok, J.; Batchvarova, N.; Kimmel, R.; Chung, P.; Zinszner, H.; Ron, D. EMBO J. 17, 3619-3630, 1998

A;Title: Identification of novel stress-induced genes downstream of chop.

A;Reference number: Z17951; MUID:98315054; PMID:9649432

A;Accession: T14271

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-2825 <WAN>

A;Cross-references: EMBL:AF059485; NID:g3170614; PID:g3170615; PIDN:AAC31807.1

C;Genetics:

A;Gene: Doc4

Query Match 96.6%; Score 14306; DB 2; Length 2825;  
Best Local Similarity 94.0%; Pred. No. 0;  
Matches 2655; Conservative 47; Mismatches 51; Indels 72; Gaps 2;

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Qy      1 MDVKERKPYRSLTRRRDAERRYSSSSADSEEGKAPQKSYSSSETLKAYDQDARLAYGSRV 60
      |||
Db      1 MDVKERKPYRSLTRRRDAERRYSSSSADSEEGKGPQKSYSSSETLKAYDQDARLAYGSRV 60

Qy     61 KDIVPQEAEEFCRTGANFTLRELGLEEVTPPHGTLYRTDIGLPHCGYSMGAGSDADMEAD 120
      ||:|||||
Db     61 KDMVPQEAEEFCRTGTNFTLRELGLGEMTPPHGTLYRTDIGLPHCGYSMGASSDADLEAD 120

Qy    121 TVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDTEHENTET----- 164
      |||
Db    121 TVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDTEHENTETGAPLHCSSASSTPIEQ 180

Qy    165 -----DHPGGL 170
      |||
Db    181 SPSPPPSPPANESQRRLGNGVAQPTPDSSEEFVPNSFLVKSGSASLGAANDHPSSL 240

Qy    171 QNHARLRTPPPLSHAHTPNQHHAASINSLNRGNFTPRSNPSPAPT D HSLSGEPPAGGAQ 230
      |||
Db    241 QNHPRLRTPPPLPHAHTPNQHHAASINSLNRGNFTPRSNPSPAPT D HSLSGEPPAGSAQ 300

Qy    231 EPAHAQENWLLNSNIPLERNLGKQPFGLGTLDNLIEMDILGASRHDGAYS DGHFLFKPG 290
      ||:|||||
Db    301 EPTHAQDNWVLNSKIPVETRNLGKQPFGLGTWQDNLIEMDIFSASRRD GAYS DGHFFFKPG 360

Qy    291 GTSPLFCTTSPGYPLTSSTVYSPPPRPLPRSTFARPAFNLKKPSKYCNWKAALSAIVIS 350
      |||
Db    361 GTSPLFCTTSPGYPLTSSTVYSPPPRPLPRSTFSRPAFNLKKPSKYCNWKAALSAILIS 420

Qy    351 ATLVILLAYFVAMHLFGLNWLQPMEG--QMYEITEDTASSWPVPTDVSLYPSGGTGLET 408
      |||
Db    421 ATLVILLAYFVAMHLFGLNWLQPMEGQM QMYEITEDTASSWPVPTDVSLYPSGGTGLET 480

Qy    409 PDRKGKGTEGKPSFFPEDSFIDSGEIDVGRRASQKIPPGTFWRSQVFI DHPVHLKFNV 468
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Db    481 PDRKGKGAAEGKPSLFPEDSFIDSGEIDVGRRASQKIPPGTFWRSQVFI DHPVHLKFNV 540

Qy    469 SLGKAALVGIYGRKGLPPSHTQFDFVELLDGRRLLTQEARSLEGTPRQSRGTVPPSSHET 528
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Db    541 SLGKAALVGIYGRKGLPPSHTQLDFVELLDGRRLLTQEARSLEGTPRQSRGTVPPSSHET 600

Qy    529 GFIQYLDSGIWHLAFYNDGKESEVVSFLT TAIESVDNCPSNCGNGDCISGTCHCFLGFL 588
      |||
Db    601 GFIQYLDSGIWHLAFYNDGKESEVVSFLT TAIESVDNCPSNCGNGDCISGTCHCFLGFL 660

Qy    589 GPDGCRASCPVLCSGNGQYMKGRCLCHSGWKAECDVPTNQCIDVACSNHGTCITGTCIC 648
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Db    661 GPDGCRASCPVLCSGNGQYMKGRCLCHSGWKAECDVPTNQCIDVACSSHGTCIMGTCIC 720

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Qy	649	NPGYKGESCEEVD CMDPTCSGRGVCVRGECHCSVGWGGTNCETPRATCLDQCSGHGTF L P	708
Db	721	NPGYKGESCEEVD CMDPTCSSRGVCVRGECHCSVGWGGTNCETPRATCLDQCSGHGTF L P	780
Qy	709	DTGLCSCDPSW TGHDCSIEICAADCGGHGVCVGGTCRCEDGWMGAACDQ RACHPRCAEHG	768
Db	781	DTGLCNCDPSW TGHDCSIEICAADCGGHGVCVGGTCRCEDGWMGAACDQ RACHPRCAEHG	840
Qy	769	TCRDGKCECSPGWNGEHCTIEGCPGLCNGNGRCTLDLNGWHCVCQLGWRGAGCDTSMETA	828
Db	841	TCRDGKCECTPGWNGEHCTIEGCPGLCNGNGRCTLDLNGWHCVCQLGWRGTGCDTSMETG	900
Qy	829	CGDSKDN DGDGLVDCMDPDCC LQPLCHINPLCLGSPNPLDI IQETQVPVVSQQNLHSFYDR	888
Db	901	CGDGKDN DGDGLVDCMDPDCC LQPLCHVNPLCLGSPDPLDI IQETQAPVVSQQNLNSFYDR	960
Qy	889	IKFLVGRDSTHIIPGENPFDGGHACVIRGQVMTSDGTPLVGVNISFVNNPLFGYTISRQD	948
Db	961	IKFLVGRDSTHSIPGENPFDGGHACVIRGQVMTSDGTPLVGVNISFINNPLFGYTISRQD	1020
Qy	949	GSFDLVTNGGISII LRFERAPFITQEHTLWLPWDRFFVMETIIMRHEENEIPSCDLSNFA	1008
Db	1021	GSFDLVTNGGISII LRFERAPFITQEHTLWLPWDRFFVMETIVMRHEENEIPSRDLSNFA	1080
Qy	1009	RPNPVVSPSPLTSFASSCAEKGPIVPEIQALQEEISISGCKMRLSYLSSRTPGYKSVLRI	1068
Db	1081	RPNPVVSPSPLTSFASSCAEKGPIVPEIQALQEEIVIAGCKMRLSYLSSRTPGYKSVVRI	1140
Qy	1069	SLTHPTIPFNLMKVHLMVAVEGR LFRKWFAAAPDLSYYFIWDKTDVYNQKVFLGSEAFVS	1128
Db	1141	SLTHPTIPFNLMKVHLMVAVEGR LFRKWFAAAPDLSYYFIWDKTDVYNQKVFLGSEAFVS	1200
Qy	1129	VG EYESCPDLILWEKRTTVLQGYEIDASKLGGWSLDKHHALNIQSGILHKGNGENQFVS	1188
Db	1201	VG EYESCPDLILWEKRTAVLQGYEIDASKLGGWSLDKHHALNIQSGILHKGNGENQFVS	1260
Qy	1189	QQPPVIGSIMGNRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYVGDFNYIRRIFFS	1248
Db	1261	QQPPVIGSIMGNRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYVGDFNYIRRIFFS	1320
Qy	1249	GNVTNILELSHSPA HKYYLATDPM SGAVFLSDSNSRRVFKIKSTVVVKDLVKNSEVVAGT	1308
Db	1321	GNVTNILEMSHSPA HKYYLATDPM SGAVFLSDTNSRRVFKVKSTTVVKDLVKNSEVVAGT	1380
Qy	1309	GDQCLPFDDTRCGDGGKATEATLTNPRGITVDKFG LIYFVDGTMIRRIDQNGIISTLLGS	1368
Db	1381	GDQCLPFDDTRCGDGGKATEATLTNPRGITVDKFG LIYFVDGTMIRRV DQNGIISTLLGS	1440
Qy	1369	NDLTSARPLSCDSVMDISQVHLEWPTDLAINPMDNSLYVL DNNVVVLQISENHQVRIVAGR	1428
Db	1441	NDLTSARPLSCDSVMEISQVRLEWPTDLAINPMDNSLYVL DNNVVVLQISENHQVRIVAGR	1500
Qy	1429	PMHCQVPGIDHFLLSKVAIHATLESATALAVSHNGVLYIAETDEKKINRIRQVTTSGEIS	1488
Db	1501	PMHCQVPGIDQFLLSKVAIHATLESATALAVSHNGVLYIAETDEKKINRIRQVTTSGEIS	1560
Qy	1489	LVAGAPSGCDCKNDANCD CFSGDDGYAKDAKLNTPSSLAVCADGELYVADLGNIRIRFIR	1548
Db	1561	LVAGAPSGCDCKNDANCD CFSGDDGYAKDAKLNTPSSLAVCADGELYVADLGNIRIRFIR	1620
Qy	1549	KNKPFLNTQNM YELSSPIDQELYLFDTTGKHLYTQSLPTGDYLYNFTYTGDGDITLITDN	1608
Db	1621	KNKPFLNTQNM YELSSPIDQELYLFDTS GKHLYTQSLPTGDYLYNFTYTGDGDITHTIDN	1680
Qy	1609	NGNMVNVR RDSTGMPLWLVPD GQVYWVTMG TNSALKSVTTQGH ELAMMTYHGNSGLLAT	1668
Db	1681	NGNMVNVR RDSTGMPLWLVPD GQVYWVTMG TNSALRSVTTQGH ELAMMTYHGNSGLLAT	1740
Qy	1669	KSNENGWTTFY EYDSFGRLTNVTFPTGQVSSFRSDT DSSVHVQVETSSKDDVTITTNLSA	1728
Db	1741	KSNENGWTTFY EYDSFGRLTNVTFPTGQVSSFRSDT DSSVHVQVETSSKDDVTITTHLSG	1800

Qy 1729 SGAFYTLQDQVRNSYYIGADGSLRLLLANGMEVALQTEPHLLAGTVNPTVGKRNVTLP I 1788  
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 Db 1801 SGAFYTLQDQVRNSYYIGADGSLRLLLANGMEVALQTEPHLLAGTVNPTVGKRNVTLP I 1860  
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 Qy 1789 DNGLNLVEWRQRKEQARGQVTVFGRRLRVHNRNLLSLDFDRVTRTEKIYDDHRKFTRLRIL 1848  
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 Db 1861 DNGLNLVEWRQRKEQARGQVTVFGRRLRVHNRNLLSLDFDRVTRTEKIYDDHRKFTRLRIL 1920  
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 Qy 1849 YDQAGRPSLWSPSSRLNGVNVITYSPGGYIAGIQRGIMSERMEYDQAGRITSRIFADGKTW 1908  
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 Db 1921 YDQAGRPSFWSPSSRLNGVNVITYSPGGHIAGIQRGIMSERMEYDQAGRITSRIFADGKMW 1980  
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 Qy 1909 SYTYLEKSMVLLHLSQRQYIFEFDKNDRLLSSVTMPNVARQTLETIRSVGYRNIYQPPEG 1968  
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 Db 1981 SYTYLEKSMVLHLHLSQRQYIFEFDKNDRLLSSVTMPNVARQTLETIRSVGYRNIYQPPEG 2040  
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 Qy 1969 NASVIQDFTEDGHLHFTFYLGTRRVIYKYGKLSKLAETLYDTTKVSFTYDETAGMLKTI 2028  
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 Db 2041 NASVIQDFTEDGHLHFTFYLGTRRVIYKYGKLSKLAETLYDTTKVSFTYDETAGMLKTV 2100  
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 Qy 2029 NLQNEGFTCTIRYRQIGPLIDRQIFRFTTEGMVNARFDYNYDNSFRVTSMQAVINETPLP 2088  
 |||||  
 Db 2101 NLQNEGFTCTIRYRQIGPLIDRQIFRFTTEGMVNARFDYNYDNSFRVTSMQAVINETPLP 2160  
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 Qy 2089 IDLYRYDDVSGKTEQFGKFGVIYYDINQIITTAVMTHTKHFDAYGRMKEVQYEIFRSLMY 2148  
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 Db 2161 IDLYRYDDVSGKTEQFGKFGVIYYDINQIITTAVMTHSKHFDAYGRMKEVQYETFRSLMY 2220  
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 Qy 2149 WMTVQYDNMGRVVKELKVGOPYANTTRYSEYDADGQLQTVSINDKPLWRYSYDLNGNLH 2208  
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 Db 2221 WMTVQYDNMGRVVKELKVGOPYANTTRYSEYDADGQLQTVSINDKPLWRYSYDLNGNLH 2280  
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 Qy 2209 LLSPGNSARLTPLRYDIRDRITRLGVDVQYKMEDEGFLRQGGDIFEYNSAGLLIKAYNRA 2268  
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 Db 2281 LLSPGNSARLTPLRYDLRDRITRLGVDVQYKMEDEGSLRQGGDVFEYNSAGLLIKAYNRA 2340  
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 Qy 2269 GSWSVRYRYDGLGRRVSSKSSSHHLQFFYADLTNP TKVTHLYNHSSEITSLYYDLQGH 2328  
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 Db 2341 GSWSVRYRYDGLGRRVSSKSSSHHLQFFYADLTNP TKVTHLYSHSSEITSLYYDLQGH 2400  
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 Qy 2329 LFAMELSSGDEFYIACDNIGTPLAVFSGTGLMIKQILYTAYGEIYMDTNP NFQIIIGYHG 2388  
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 Db 2401 LFAMELSSGDEFYIACDNIGTPLAVFSGTGLMIKQILYTAYGEIYMDTNP NFQIIIGYHG 2460  
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 Qy 2389 GLYDPLTKLVHMGRRDYDVLAGRWTSPDH ELWKHLSSSNVMPFNLYMFKNNNPISNSQDI 2448  
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 Db 2461 GLYDPLTKLVHMGRRDYDVLAGRWTSPDH ELWKRLSSNSIVPFHLYMFKNNNPISNSQDI 2520  
 |||||  
 Qy 2449 KCFMTDVNSWLLTFGFLHNVIPGYPKPDM DAMEPSYELIHTQMKTQEWDNSKSILGVQC 2508  
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 Db 2521 KCFMTDVNSWLLTFGFLHNVIPGYPKPDT DAMEPSYELVHTQMKTQEWDNSKSILGVQC 2580  
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 Qy 2509 EVQKQLKAFVTLERFDQLYGSTITSCQAPKTKKFASSGSVFGKGVK FALKDGRVTTDII 2568  
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 Db 2581 EVQKQLKAFVTLERFDQLYGSTITSCQAPETKKFASSGSIFGKGVK FALKDGRVTTDII 2640  
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 Qy 2569 SVANEDGRRVAAILNHAHYLENLHFTIDGV DTHYFVKPGPSEGLAILGLSGGRRTLENG 2628  
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 Db 2641 SVANEDGRRIAAILNNAHYLENLHFTIDGV DTHYFVKPGPSEGLAILGLSGGRRTLENG 2700  
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 Qy 2629 VNVTVSQINTVLNGRTRRYTDIQLQY GALCLNTRYGTTLDEEKARVLELARQAVRQAWA 2688  
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 Db 2701 VNVTVSQINTMLSGRTRRYTDIQLQY RALCLNTRYGTTVDEEKVRVLELARQAVRQAWA 2760  
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 Qy 2689 REQQRLREGEGLRAWTEGEKQVVLSTGRVQGYDGF FVISVEQYPELSDSANNIHFMRQS 2748  
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 Db 2761 REQQRLREGEGLRAWTDGEKQVVLNTRGVQGYDGF FVTSVEQYPELSDSANNIHFMRQS 2820  
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 Qy 2749 EMGRR 2753  
 |||||

Db 2821 EMGRR 2825